

In the Specification:

Please amend the paragraph at page 6, lines 12-15, as follows:

~~Figure 5 shows~~ Figures 5A – 5C show the amino acid sequence for the GAS36 homologs with the histidine triad regions underlined (~~Fig. 5(a) and (b)~~ Figs. 5A and 5B) and the sequence for a GBS36 homolog (~~Fig. 5(c)~~ Fig. 5C) with its histidine triad regions underlined.

At page 28, please amend the paragraph beginning at line 13, as follows:

Sequence comparisons of the Sp36 encoded protein sequence against the publicly available GenBank sequence database (including the unfinished microbial database) revealed two highly homologous amino acid sequences. One of these was a predicted amino acid sequence from the *S. pyogenes* genome. This predicted polypeptide comprised 825 amino acid residues (MW = 92,616 Da) that was 25.1% identical to the Sp36 amino acid sequence from pneumococcus serotype 4 but maintained the 5 histidine triads (underlined in Figure 5(a) 5A - SEQ ID NO: 2). The second polypeptide encoded within the *S. pyogenes* database contained several errors that were corrected by our sequencing of this region of the genome. The DNA fragment obtained encoded a protein of 792 amino acids (MW = 87,457 Da) that was 12.6% identical to the pneumococcal sequence and 12.5% identical to the first *S. pyogenes* polypeptide. This predicted amino acid sequence contained four histidine triad motifs (underlined in Fig. 5(b) 5B – SEQ ID NO.: 4). The third polypeptide sequence obtained was one already in the database (Accession No. AF062533) and identified only as an unknown gene downstream from a gene identified as *lmb* in *S. galactiae*. This 822 amino acid protein thus has a predicted molecular weight of 92,353 Da and maintains the 5 histidine triad motifs (underlined in Figure 5(c) 5C - SEQ ID NO: 6). This second polypeptide shows 25.6% sequence identity

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to Sp36 of pneumococcus type 4 and 97.7% and 11.6% identity to the two group A homologs, respectively.